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1645

## RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/09/966,781A

TIME: 14:26:05

Input Set : A:\A281us11.app

Output Set: N:\CRF3\02112002\I966781A.raw

ENTERED

3 <110> APPLICANT: SOULARD, PATRICIA  
 5 <120> TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR  
 6 SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY  
 8 <130> FILE REFERENCE: A0000281US  
 10 <140> CURRENT APPLICATION NUMBER: 09/966781A  
 11 <141> CURRENT FILING DATE: 2001-09-28  
 13 <150> PRIOR APPLICATION NUMBER: EP004026837  
 14 <151> PRIOR FILING DATE: 2000-09-28  
 16 <160> NUMBER OF SEQ ID NOS: 35  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 426  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Homo sapiens  
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 29 Ser Arg Ala Gly Phe Glu Ser Glu Arg Arg Gly Ser His Pro Tyr Ile  
 30 20 25 30  
 32 Asp Phe Arg Ile Phe His Ser Gln Ser Glu Ile Glu Val Ser Val Ser  
 33 35 40 45  
 35 Ala Arg Asn Ile Arg Arg Leu Leu Ser Phe Gln Arg Tyr Leu Arg Ser  
 36 50 55 60  
 38 Ser Arg Phe Phe Arg Gly Thr Ala Val Ser Asn Ser Leu Asn Ile Leu  
 39 65 70 75 80  
 41 Asp Asp Asp Tyr Asn Gly Gln Ala Lys Cys Met Leu Glu Lys Val Gly  
 42 85 90 95  
 44 Asn Trp Asn Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn  
 45 100 105 110  
 47 Ser Leu Val Ser Leu Thr Phe His Leu Phe Ser Leu His Gly Leu Ile  
 48 115 120 125  
 50 Glu Tyr Phe His Leu Asp Met Met Lys Leu Arg Arg Phe Leu Val Met  
 51 130 135 140  
 53 Ile Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val His  
 54 145 150 155 160  
 56 Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro Lys  
 57 165 170 175  
 59 Leu Ala Asn Ser Val Thr Pro Trp Asp Ile Leu Leu Ser Leu Ile Ala  
 60 180 185 190  
 62 Ala Ala Thr His Asp Leu Asp His Pro Gly Val Asn Gln Pro Phe Leu  
 63 195 200 205  
 65 Ile Lys Thr Asn His Tyr Leu Ala Thr Leu Tyr Lys Asn Thr Ser Val  
 66 210 215 220

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68 Leu Glu Asn His His Trp Arg Ser Ala Val Gly Leu Leu Arg Glu Ser
69 225                230                235                240
71 Gly Leu Phe Ser His Leu Pro Leu Glu Ser Arg Gln Gln Met Glu Thr
72                245                250                255
74 Gln Ile Gly Ala Leu Ile Leu Ala Thr Asp Ile Ser Arg Gln Asn Glu
75                260                265                270
77 Tyr Leu Ser Leu Phe Arg Ser His Leu Asp Arg Gly Asp Leu Cys Leu
78                275                280                285
80 Glu Asp Thr Arg His Arg His Leu Val Leu Gln Met Ala Leu Lys Cys
81                290                295                300
83 Ala Asp Ile Cys Asn Pro Cys Arg Thr Trp Glu Leu Ser Lys Gln Trp
84 305                310                315                320
86 Ser Glu Lys Val Thr Glu Glu Phe Phe His Gln Gly Asp Ile Glu Lys
87                325                330                335
89 Lys Tyr His Leu Gly Val Ser Pro Leu Cys Asp Arg His Thr Glu Ser
90                340                345                350
92 Ile Ala Asn Ile Gln Ile Gly Phe Met Thr Tyr Leu Val Glu Pro Leu
93                355                360                365
95 Phe Thr Glu Trp Ala Arg Phe Ser Asn Thr Arg Leu Ser Gln Thr Met
96                370                375                380
98 Leu Gly His Val Gly Leu Asn Lys Ala Ser Trp Lys Gly Leu Gln Arg
99 385                390                395                400
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108 <210> SEQ ID NO: 2
109 <211> LENGTH: 426
110 <212> TYPE: PRT
111 <213> ORGANISM: Mus sp.
113 <400> SEQUENCE: 2
114 Asp Gln Thr Ala Leu Tyr Ile Arg Met Leu Gly Asp Val Arg Val Arg
115 1                5                10                15
117 Ser Arg Ala Gly Phe Glu Thr Glu Arg Arg Gly Ser His Pro Tyr Ile
118                20                25                30
120 Asp Phe Arg Ile Phe His Ser Gln Ser Asp Ile Glu Ala Ser Val Ser
121                35                40                45
123 Ala Arg Asn Ile Arg Arg Leu Ser Phe Gln Arg Tyr Leu Arg Ser
124                50                55                60
126 Ser Arg Val Phe Arg Gly Ala Thr Val Cys Ser Ser Leu Asp Ile Leu
127 65                70                75                80
129 Asp Glu Asp Tyr Asn Gly Gln Ala Lys Cys Met Leu Glu Lys Val Gly
130                85                90                95
132 Asn Trp Asn Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn
133                100                105                110
135 Ser Leu Val Ser Leu Thr Phe His Leu Phe Ser Leu His Gly Leu Ile
136                115                120                125
138 Glu Tyr Phe His Leu Asp Met Val Lys Leu Arg Arg Phe Leu Val Met
139                130                135                140

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141 Ile Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val His
142 145                               150                               155                               160
144 Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro Lys
145                               165                               170                               175
147 Leu Ala Ser Ser Val Thr Pro Trp Asp Ile Leu Leu Ser Leu Ile Ala
148                               180                               185                               190
150 Ala Ala Thr His Asp Leu Asp His Pro Gly Val Asn Gln Pro Phe Leu
151                               195                               200                               205
153 Ile Lys Thr Asn His Tyr Leu Ala Thr Leu Tyr Lys Asn Ser Ser Val
154                               210                               215                               220
156 Leu Glu Asn His His Trp Arg Ser Ala Val Gly Leu Leu Arg Glu Ser
157 225                               230                               235                               240
159 Gly Leu Phe Ser His Leu Pro Leu Glu Ser Arg Gln Glu Met Glu Ala
160                               245                               250                               255
162 Gln Ile Gly Ala Leu Ile Leu Ala Thr Asp Ile Ser Arg Gln Asn Glu
163                               260                               265                               270
165 Tyr Leu Ser Leu Phe Arg Ser His Leu Asp Lys Gly Asp Leu His Leu
166                               275                               280                               285
168 Asp Asp Gly Arg His Arg His Leu Val Leu Gln Met Ala Leu Lys Cys
169                               290                               295                               300
171 Ala Asp Ile Cys Asn Pro Cys Arg Asn Trp Glu Leu Ser Lys Gln Trp
172 305                               310                               315                               320
174 Ser Glu Lys Val Thr Glu Glu Phe Phe His Gln Gly Asp Ile Glu Lys
175                               325                               330                               335
177 Lys Tyr His Leu Gly Val Ser Pro Leu Cys Asp Arg Gln Thr Glu Ser
178                               340                               345                               350
180 Ile Ala Asn Ile Gln Ile Gly Phe Met Thr Tyr Leu Val Glu Pro Leu
181                               355                               360                               365
183 Phe Thr Glu Trp Ala Arg Phe Ser Ala Thr Arg Leu Ser Gln Thr Met
184                               370                               375                               380
186 Leu Gly His Val Gly Leu Asn Lys Ala Ser Trp Lys Gly Leu Gln Arg
187 385                               390                               395                               400
189 Gln Gln Pro Ser Ser Glu Asp Ala Asn Ala Ala Phe Glu Leu Asn Ser
190                               405                               410                               415
192 Gln Leu Leu Thr Gln Glu Asn Arg Leu Ser
193                               420                               425
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 426
198 <212> TYPE: PRT
199 <213> ORGANISM: Rattus sp.
201 <400> SEQUENCE: 3
202 Asp Gln Thr Ala Leu Tyr Ile Arg Met Leu Gly Asp Val Arg Val Arg
203 1                               5                               10                               15
205 Ser Arg Ala Gly Phe Glu Thr Glu Arg Arg Gly Ser His Pro Tyr Ile
206                               20                               25                               30
208 Asp Phe Arg Ile Phe His Ala Gln Ser Glu Ile Glu Ala Ser Val Ser
209                               35                               40                               45
211 Ala Arg Asn Ile Arg Arg Leu Leu Ser Phe Gln Arg Tyr Leu Arg Ser
212                               50                               55                               60

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Output Set: N:\CRF3\02112002\I966781A.raw

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214 Ser Arg Phe Phe Arg Gly Ala Thr Val Cys Arg Ser Leu Asn Ile Leu
215 65 70 75 80
217 Asp Glu Asp Tyr Asn Gly Gln Ala Lys Cys Met Leu Glu Lys Val Gly
218 85 90 95
220 Asn Trp Asn Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn
221 100 105 110
223 Ser Leu Val Ser Leu Thr Phe His Leu Phe Ser Leu His Gly Leu Ile
224 115 120 125
226 Glu Tyr Phe His Leu Asp Met Val Lys Leu Arg Arg Phe Leu Val Met
227 130 135 140
229 Ile Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val His
230 145 150 155 160
232 Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro Lys
233 165 170 175
235 Leu Ala Asn Ser Val Thr Pro Trp Asp Ile Leu Leu Ser Leu Ile Ala
236 180 185 190
238 Ala Ala Thr His Asp Leu Asp His Pro Gly Val Asn Gln Pro Phe Leu
239 195 200 205
241 Ile Lys Thr Asn His Tyr Leu Ala Thr Leu Tyr Lys Asn Thr Ser Val
242 210 215 220
244 Leu Glu Asn His His Trp Arg Ser Ala Val Gly Leu Leu Arg Glu Ser
245 225 230 235 240
247 Gly Leu Phe Ser His Leu Pro Leu Glu Ser Arg His Glu Met Glu Ala
248 245 250 255
250 Gln Ile Gly Ala Leu Ile Leu Ala Thr Asp Ile Ser Arg Gln Asn Glu
251 260 265 270
253 Tyr Leu Ser Leu Phe Arg Ser His Leu Asp Lys Gly Asp Leu His Leu
254 275 280 285
256 Asp Asp Gly Arg His Arg His Leu Val Leu Gln Met Ala Leu Lys Cys
257 290 295 300
259 Ala Asp Ile Cys Asn Pro Cys Arg Asn Trp Glu Leu Ser Lys Gln Trp
260 305 310 315 320
262 Ser Glu Lys Val Thr Glu Glu Phe Phe His Gln Gly Asp Ile Glu Lys
263 325 330 335
265 Lys Tyr His Leu Gly Val Ser Pro Leu Cys Asp Arg Gln Thr Glu Ser
266 340 345 350
268 Ile Ala Asn Ile Gln Ile Gly Phe Met Thr Tyr Leu Gln Glu Pro Leu
269 355 360 365
271 Phe Thr Glu Trp Ala Arg Phe Ser Asp Thr Arg Leu Ser Gln Thr Met
272 370 375 380
274 Leu Gly His Val Gly Leu Asn Lys Ala Ser Trp Lys Gly Leu Gln Arg
275 385 390 395 400
277 Gln Gln Pro Ser Ser Glu Asp Ala Ser Ala Ala Phe Glu Leu Asn Ser
278 405 410 415
280 Gln Leu Leu Thr Gln Glu Asn Arg Leu Ser
281 420 425
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 1281
286 <212> TYPE: DNA

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TIME: 14:26:05

Input Set : A:\A281us11.app

Output Set: N:\CRF3\02112002\I966781A.raw

287 &lt;213&gt; ORGANISM: Homo sapiens

289 &lt;400&gt; SEQUENCE: 4

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290 gatcagactg cattatacat tcgtatgcta ggagatgtac gtgtaaggag ccgagcagga 60
291 tttgaatcag aaagaagagg ttctcaccca tatattgatt ttcgtatitt ccactctcaa 120
292 tctgaaattg aagtgtctgt ctctgcaagg aatatcagaa ggctactaag tttccagcga 180
293 tatcttagat cttcacgctt ttttcgtggt actgcggttt caaattccct aaacatttta 240
294 gatgatgatt ataattggaca agccaagtgt atgctggaaa aagttggaaa ttggaatttt 300
295 gatatctttc tatttgatag actaaccat ggaaatagtc tagtaagctt aacctttcat 360
296 ttatttagtc ttcatggatt aattgagtac ttccatttag atatgatgaa acttcgtaga 420
297 tttttagtta tgattcaaga agattaccac agtcaaaaatc cttaccataa cgcagtcac 480
298 gctgcggatg ttactcaggc catgcaactgt tacttaaaagg aacctaaagct tgccaattct 540
299 gtaactcctt gggatatctt gctgagctta attgcagctg ccactcatga tctggatcat 600
300 ccagggtgta atcaaccttt cttattaaa actaaccatt acttggcaac tttatacaag 660
301 aataacctcag tactggaaaa tcaccactgg agatctgcag tgggcttatt gagagaatca 720
302 ggcttattct cacatctgcc attagaaaagc aggcaacaaa tggagacaca gataggtgct 780
303 ctgatactag ccacagacat cagtcgccag aatgagtatc tgtctttgtt taggtcccat 840
304 ttggatagag gtgatttatg cctagaagac accagacaca gacatttggt tttacagatg 900
305 gctttgaaat gtgctgatat ttgtaaccca tgcggacgt gggaaattaag caagcagtg 960
306 agtgaaaaag taacggagga attcttccat caaggagata tagaaaaaaa atatcatttg 1020
307 ggtgtgagtc cactttgcga tcgtcacact gaatctattg ccaacatcca gattggtttt 1080
308 atgacttacc tagtggagcc tttatttaca gaatgggcca ggttttccaa tacaaggcta 1140
309 tcccagacaa tgcttgga cgtggggctg aataaagcca gctggaaggg actgcagaga 1200
310 gaacagtcga gcagtga cactgatgct gcatttgagt tgaactcaca gttattacct 1260
311 caggaaaatc ggttatcata a

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1281

314 &lt;210&gt; SEQ ID NO: 5

315 &lt;211&gt; LENGTH: 1281

316 &lt;212&gt; TYPE: DNA

317 &lt;213&gt; ORGANISM: Mus sp.

319 &lt;400&gt; SEQUENCE: 5

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320 gatcagactg cattatacat tcgtatgcta ggagatgtac gtgtaaggag ccgagcagga 60
321 tttgaatcag aaagaagagg ttctcaccca tatattgatt ttcgtatitt ccactctcaa 120
322 tctgaaattg aagtgtctgt ctctgcaagg aatatcagaa ggctactaag tttccagcga 180
323 tatcttagat cttcacgctt ttttcgtggt actgcggttt caaattccct aaacatttta 240
324 gatgatgatt ataattggaca agccaagtgt atgctggaaa aagttggaaa ttggaatttt 300
325 gatatctttc tatttgatag actaaccat ggaaatagtc tagtaagctt aacctttcat 360
326 ttatttagtc ttcatggatt aattgagtac ttccatttag atatgatgaa acttcgtaga 420
327 tttttagtta tgattcaaga agattaccac agtcaaaaatc cttaccataa cgcagtcac 480
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329 gtaactcctt gggatatctt gctgagctta attgcagctg ccactcatga tctggatcat 600
330 ccagggtgta atcaaccttt cttattaaa actaaccatt acttggcaac tttatacaag 660
331 aataacctcag tactggaaaa tcaccactgg agatctgcag tgggcttatt gagagaatca 720
332 ggcttattct cacatctgcc attagaaaagc aggcaacaaa tggagacaca gataggtgct 780
333 ctgatactag ccacagacat cagtcgccag aatgagtatc tgtctttgtt taggtcccat 840
334 ttggatagag gtgatttatg cctagaagac accagacaca gacatttggt tttacagatg 900
335 gctttgaaat gtgctgatat ttgtaaccca tgcggacgt gggaaattaag caagcagtg 960
336 agtgaaaaag taacggagga attcttccat caaggagata tagaaaaaaa atatcatttg 1020
337 ggtgtgagtc cactttgcga tcgtcacact gaatctattg ccaacatcca gattggtttt 1080
338 atgacttacc tagtggagcc tttatttaca gaatgggcca ggttttccaa tacaaggcta 1140
339 tcccagacaa tgcttgga cgtggggctg aataaagcca gctggaaggg actgcagaga 1200

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## VERIFICATION SUMMARY

DATE: 02/11/2002

PATENT APPLICATION: US/09/966,781A

TIME: 14:26:06

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L:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
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